Does Not Comply
Corrected Diskette Needed

PCT09

RAW SEQUENCE LISTING   DATE: 10/01/2002
PATENT APPLICATION: US/09/913,770   TIME: 10:56:44

Input Set : A:\2590SEQ.txt
Output Set: N:\CRF4\10012002\I913770.raw

```
        2 <110> APPLICANT: Takeda Chemical Industries, Ltd.
W-->    3 <120> TITLE OF INVENTION: Novel G Protein Coupled Receptor Protein and Its DNA
W-->    4 <130> FILE REFERENCE: 2590WOOP
C-->    5 <140> CURRENT APPLICATION NUMBER: US/09/913,770
C-->    5 <141> CURRENT FILING DATE: 2001-08-17
        5 <150> PRIOR APPLICATION NUMBER: JP 11-041336
        6 <151> PRIOR FILING DATE: 1999-02-19
        7 <150> PRIOR APPLICATION NUMBER: JP 11-125768
        8 <151> PRIOR FILING DATE: 1999-05-06
W-->    9 <160> NUMBER OF SEQ ID: 4
```

ERRORED SEQUENCES

```
       90 <210> SEQ ID NO: 4
       91 <211> LENGTH: 25
       92 <212> TYPE: DNA
       93 <213> ORGANISM: Artificial Sequence          See items || an Error Summary
W-->   94 <220> FEATURE:                                                    Sheet
       95 <223> OTHER INFORMATION:
W-->   96 <400> SEQUENCE: 4
C-->   97 ctaaaagtgt gatttcagag tgttt
E-->   98 1/4
```

delete   all bases Must be in Lower-case Letters,
                        when using
                        new Sequence
                        Rules format

VERIFICATION SUMMARY　　　　　　　　　DATE: 10/01/2002
PATENT APPLICATION: US/09/913,770　　　TIME: 10:56:45

Input Set : **A:\2590SEQ.txt**
Output Set: **N:\CRF4\10012002\I913770.raw**

```
L:3 M:283 W: Missing Blank Line separator, <120> field identifier
L:4 M:283 W: Missing Blank Line separator, <130> field identifier
L:5 M:270 C: Current Application Number differs, Replaced Current Application No
L:5 M:271 C: Current Filing Date differs, Replaced Current Filing Date
L:9 M:283 W: Missing Blank Line separator, <160> field identifier
L:10 M:283 W: Missing Blank Line separator, <210> field identifier
L:14 M:283 W: Missing Blank Line separator, <400> field identifier
L:63 M:283 W: Missing Blank Line separator, <400> field identifier
L:64 M:112 C: (48) String data converted to lower case,
M:112 Repeated in SeqNo=2
L:86 M:283 W: Missing Blank Line separator, <220> field identifier
L:88 M:283 W: Missing Blank Line separator, <400> field identifier
L:89 M:112 C: (48) String data converted to lower case,
L:94 M:283 W: Missing Blank Line separator, <220> field identifier
L:96 M:283 W: Missing Blank Line separator, <400> field identifier
L:97 M:112 C: (48) String data converted to lower case,
L:98 M:254 E: No. of Bases conflict, LENGTH:Input:4 Counted:26 SEQ:4
L:98 M:320 E: (1) Wrong Nucleic Acid Designator, NUMBER OF INVALID KEYS:2
L:98 M:252 E: No. of Seq. differs, <211> LENGTH:Input:25 Found:26 SEQ:4
```